

SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Method for identifying compounds that modulate sister chromatid separation

<130> 0652.2290001

<140> To be assigned

<141> Herewith

<150> EP 01 101 252.3

<151> 2001-01-19

<150> US 60/297,440

<151> 2001-06-13

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 6668

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

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<222> (145)..(6507)

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Pro Glu Lys Glu Ser Phe Gln Glu Arg Leu Ala Leu Ile Pro Ser Gly	
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gtg act gtg tgt gtg ttg gcc ctg gcc acc ctc cag ccc gga acc gtg	5307
Val Thr Val Cys Val Leu Ala Leu Ala Thr Leu Gln Pro Gly Thr Val	
1710 1715 1720	
ggc aac acc ctc ctg ctg acc cgg ctg gaa aag gac agt ccc cca gtc	5355
Gly Asn Thr Leu Leu Leu Thr Arg Leu Glu Lys Asp Ser Pro Pro Val	
1725 1730 1735	
agt gtg cag att ccc act ggc cag aac aag ctt cat ctg cgt tca gtc	5403
Ser Val Gln Ile Pro Thr Gly Gln Asn Lys Leu His Leu Arg Ser Val	
1740 1745 1750	
ctg aat gag ttt gat gcc atc cag aag gca cag aaa gag aac agc agc	5451
Leu Asn Glu Phe Asp Ala Ile Gln Lys Ala Gln Lys Glu Asn Ser Ser	
1755 1760 1765	
tgt act gac aag cga gaa tgg tgg aca ggg cgg ctg gca ctg gac cac	5499
Cys Thr Asp Lys Arg Glu Trp Trp Thr Gly Arg Leu Ala Leu Asp His	
1770 1775 1780 1785	
agg atg gag gtt ctc atc gct tcc cta gag aag tct gtg ctg ggc tgc	5547
Arg Met Glu Val Leu Ile Ala Ser Leu Glu Lys Ser Val Leu Gly Cys	
1790 1795 1800	
tgg aag ggg ctg ctg ctg ccg tcc agt gag gag ccc ggc cct gcc cag	5595
Trp Lys Gly Leu Leu Leu Pro Ser Ser Glu Glu Pro Gly Pro Ala Gln	

1805	1810	1815	
gag gcc tcc cgc cta cag gag ctg cta cag gac tgt ggc tgg aaa tat Glu Ala Ser Arg Leu Gln Glu Leu Leu Gln Asp Cys Gly Trp Lys Tyr 1820 1825 1830			5643
cct gac cgc act ctg ctg aaa atc atg ctc agt ggt gcc ggt gcc ctc Pro Asp Arg Thr Leu Leu Lys Ile Met Leu Ser Gly Ala Gly Ala Leu 1835 1840 1845			5691
acc cct cag gac att cag gcc ctg gcc tac ggg ctg tgc cca acc cag Thr Pro Gln Asp Ile Gln Ala Leu Ala Tyr Gly Leu Cys Pro Thr Gln 1850 1855 1860 1865			5739
cca gag cga gcc cag gag ctc ctg aat gag gca gta gga cgt cta cag Pro Glu Arg Ala Gln Glu Leu Leu Asn Glu Ala Val Gly Arg Leu Gln 1870 1875 1880			5787
ggc ctg aca gta cca agc aat agc cac ctt gtc ttg gtc cta gac aag Gly Leu Thr Val Pro Ser Asn Ser His Leu Val Leu Val Leu Asp Lys 1885 1890 1895			5835
gac ttg cag aag ctg ccg tgg gaa agc atg ccc agc ctc caa gca ctg Asp Leu Gln Lys Leu Pro Trp Glu Ser Met Pro Ser Leu Gln Ala Leu 1900 1905 1910			5883
cct gtc acc cgg ctg ccc tcc ttc cgc ttc cta ctc agc tac tcc atc Pro Val Thr Arg Leu Pro Ser Phe Arg Phe Leu Leu Ser Tyr Ser Ile 1915 1920 1925			5931
atc aaa gag tat ggg gcc tcg cca gtg ctg agt caa ggg gtg gat cca Ile Lys Glu Tyr Gly Ala Ser Pro Val Leu Ser Gln Gly Val Asp Pro 1930 1935 1940 1945			5979
cga agt acc ttc tat gtc ctg aac cct cac aat aac ctg tca agc aca Arg Ser Thr Phe Tyr Val Leu Asn Pro His Asn Asn Leu Ser Ser Thr 1950 1955 1960			6027
gag gag caa ttt cga gcc aat ttc agc agt gaa gct ggc tgg aga gga Glu Glu Gln Phe Arg Ala Asn Phe Ser Ser Glu Ala Gly Trp Arg Gly 1965 1970 1975			6075
gtg gtt ggg gag gtg cca aga cct gaa cag gtg cag gaa gcc ctg aca Val Val Gly Glu Val Pro Arg Pro Glu Gln Val Gln Glu Ala Leu Thr 1980 1985 1990			6123
aag cat gat ttg tat atc tat gca ggg cat ggg gct ggt gcc cgc ttc Lys His Asp Leu Tyr Ile Tyr Ala Gly His Gly Ala Gly Ala Arg Phe 1995 2000 2005			6171
ctt gat ggg cag gct gtc ctg cgg ctg agc tgt cgg gca gtg gcc ctg Leu Asp Gly Gln Ala Val Leu Arg Leu Ser Cys Arg Ala Val Ala Leu 2010 2015 2020 2025			6219
ctg ttt ggc tgt agc agt gcg gcc ctg gct gtg cat gga aac ctg gag Leu Phe Gly Cys Ser Ser Ala Ala Leu Ala Val His Gly Asn Leu Glu 2030 2035 2040			6267
ggg gct ggc atc gtg ctc aag tac atc atg gct ggt tgc ccc ttg ttt Gly Ala Gly Ile Val Leu Lys Tyr Ile Met Ala Gly Cys Pro Leu Phe 2045 2050 2055			6315

Arg Arg Ala Ala Phe Ala Ala Arg Leu Lys Ala Leu Ser Phe Leu Val
165 170 175

Leu Leu Glu Asp Glu Ser Thr Pro Cys Glu Val Pro His Phe Ala Ser
 180 185 190
 Pro Thr Ala Cys Arg Ala Val Ala Ala His Gln Leu Phe Asp Ala Ser
 195 200 205
 Gly His Gly Leu Asn Glu Ala Asp Ala Asp Phe Leu Asp Asp Leu Leu
 210 215 220
 Ser Arg His Val Ile Arg Ala Leu Val Gly Glu Arg Gly Ser Ser Ser
 225 230 235 240
 Gly Leu Leu Ser Pro Gln Arg Ala Leu Cys Leu Leu Glu Leu Thr Leu
 245 250 255
 Glu His Cys Arg Arg Phe Cys Trp Ser Arg His His Asp Lys Ala Ile
 260 265 270
 Ser Ala Val Glu Lys Ala His Ser Tyr Leu Arg Asn Thr Asn Leu Ala
 275 280 285
 Pro Ser Leu Gln Leu Cys Gln Leu Gly Val Lys Leu Leu Gln Val Gly
 290 295 300
 Glu Glu Gly Pro Gln Ala Val Ala Lys Leu Leu Ile Lys Ala Ser Ala
 305 310 315 320
 Val Leu Ser Lys Ser Met Glu Ala Pro Ser Pro Pro Leu Arg Ala Leu
 325 330 335
 Tyr Glu Ser Cys Gln Phe Phe Leu Ser Gly Leu Glu Arg Gly Thr Lys
 340 345 350
 Arg Arg Tyr Arg Leu Asp Ala Ile Leu Ser Leu Phe Ala Phe Leu Gly
 355 360 365
 Gly Tyr Cys Ser Leu Leu Gln Gln Leu Arg Asp Asp Gly Val Tyr Gly
 370 375 380
 Gly Ser Ser Lys Gln Gln Gln Ser Phe Leu Gln Met Tyr Phe Gln Gly
 385 390 395 400
 Leu His Leu Tyr Thr Val Val Val Tyr Asp Phe Ala Gln Gly Cys Gln
 405 410 415
 Ile Val Asp Leu Ala Asp Leu Thr Gln Leu Val Asp Ser Cys Lys Ser
 420 425 430
 Thr Val Val Trp Met Leu Glu Ala Leu Glu Gly Leu Ser Gly Gln Glu
 435 440 445
 Leu Thr Asp His Met Gly Met Thr Ala Ser Tyr Thr Ser Asn Leu Ala
 450 455 460
 Tyr Ser Phe Tyr Ser His Lys Leu Tyr Ala Glu Ala Cys Ala Ile Ser
 465 470 475 480
 Glu Pro Leu Cys Gln His Leu Gly Leu Val Lys Pro Gly Thr Tyr Pro
 485 490 495
 Glu Val Pro Pro Glu Lys Leu His Arg Cys Phe Arg Leu Gln Val Glu
 500 505 510

Ser	Leu	Lys	Lys	Leu	Gly	Lys	Gln	Ala	Gln	Gly	Cys	Lys	Met	Val	Ile		
		515					520					525					
Leu	Trp	Leu	Ala	Ala	Leu	Gln	Pro	Cys	Ser	Pro	Glu	His	Met	Ala	Glu		
	530					535					540						
Pro	Val	Thr	Phe	Trp	Val	Arg	Val	Lys	Met	Asp	Ala	Ala	Arg	Ala	Gly		
545					550					555					560		
Asp	Lys	Glu	Leu	Gln	Leu	Lys	Thr	Leu	Arg	Asp	Ser	Leu	Ser	Gly	Trp		
				565					570					575			
Asp	Pro	Glu	Thr	Leu	Ala	Leu	Leu	Leu	Arg	Glu	Glu	Leu	Gln	Ala	Tyr		
			580						585				590				
Lys	Ala	Val	Arg	Ala	Asp	Thr	Gly	Gln	Glu	Arg	Phe	Asn	Ile	Ile	Cys		
		595					600					605					
Asp	Leu	Leu	Glu	Leu	Ser	Pro	Glu	Glu	Thr	Pro	Ala	Gly	Ala	Trp	Ala		
	610					615					620						
Arg	Ala	Thr	His	Leu	Val	Glu	Leu	Ala	Gln	Val	Leu	Cys	Tyr	His	Asp		
625					630					635					640		
Phe	Thr	Gln	Gln	Thr	Asn	Cys	Ser	Ala	Leu	Asp	Ala	Ile	Arg	Glu	Ala		
				645					650					655			
Leu	Gln	Leu	Leu	Asp	Ser	Val	Arg	Pro	Glu	Ala	Gln	Ala	Arg	Asp	Gln		
			660					665					670				
Leu	Leu	Asp	Asp	Lys	Ala	Gln	Ala	Leu	Leu	Trp	Leu	Tyr	Ile	Cys	Thr		
		675					680					685					
Leu	Glu	Ala	Lys	Ile	Gln	Glu	Gly	Ile	Glu	Arg	Asp	Arg	Arg	Ala	Gln		
	690					695					700						
Ala	Pro	Gly	Asn	Leu	Glu	Glu	Phe	Glu	Val	Asn	Asp	Leu	Asn	Tyr	Glu		
705					710					715					720		
Asp	Lys	Leu	Gln	Glu	Asp	Arg	Phe	Leu	Tyr	Ser	Asn	Ile	Ala	Phe	Asn		
				725					730					735			
Leu	Ala	Ala	Asp	Ala	Ala	Gln	Ser	Lys	Cys	Leu	Asp	Gln	Ala	Leu	Ala		
			740					745					750				
Leu	Trp	Lys	Glu	Leu	Leu	Thr	Lys	Gly	Gln	Ala	Pro	Ala	Val	Arg	Cys		
		755					760					765					
Leu	Gln	Gln	Thr	Ala	Ala	Ser	Leu	Gln	Ile	Leu	Ala	Ala	Leu	Tyr	Gln		
	770					775					780						
Leu	Val	Ala	Lys	Pro	Met	Gln	Ala	Leu	Glu	Val	Leu	Leu	Leu	Leu	Arg		
785					790					795					800		
Ile	Val	Ser	Glu	Arg	Leu	Lys	Asp	His	Ser	Lys	Ala	Ala	Gly	Ser	Ser		
				805					810					815			
Cys	His	Ile	Thr	Gln	Leu	Leu	Leu	Thr	Leu	Gly	Cys	Pro	Ser	Tyr	Ala		
			820					825					830				
Gln	Leu	His	Leu	Glu	Glu	Ala	Ala	Ser	Ser	Leu	Lys	His	Leu	Asp	Gln		

835					840					845					
Thr	Thr	Asp	Thr	Tyr	Leu	Leu	Leu	Ser	Leu	Thr	Cys	Asp	Leu	Leu	Arg
	850					855					860				
Ser	Gln	Leu	Tyr	Trp	Thr	His	Gln	Lys	Val	Thr	Lys	Gly	Val	Ser	Leu
865					870					875					880
Leu	Leu	Ser	Val	Leu	Arg	Asp	Pro	Ala	Leu	Gln	Lys	Ser	Ser	Lys	Ala
				885					890					895	
Trp	Tyr	Leu	Leu	Arg	Val	Gln	Val	Leu	Gln	Leu	Val	Ala	Ala	Tyr	Leu
		900						905					910		
Ser	Leu	Pro	Ser	Asn	Asn	Leu	Ser	His	Ser	Leu	Trp	Glu	Gln	Leu	Cys
		915					920					925			
Ala	Gln	Gly	Trp	Gln	Thr	Pro	Glu	Ile	Ala	Leu	Ile	Asp	Ser	His	Lys
	930					935					940				
Leu	Leu	Arg	Ser	Ile	Ile	Leu	Leu	Leu	Met	Gly	Ser	Asp	Ile	Leu	Ser
945					950					955					960
Thr	Gln	Lys	Ala	Ala	Val	Glu	Thr	Ser	Phe	Leu	Asp	Tyr	Gly	Glu	Asn
				965					970					975	
Leu	Val	Gln	Lys	Trp	Gln	Val	Leu	Ser	Glu	Val	Leu	Ser	Cys	Ser	Glu
			980					985					990		
Lys	Leu	Val	Cys	His	Leu	Gly	Arg	Leu	Gly	Ser	Val	Ser	Glu	Ala	Lys
		995					1000					1005			
Ala	Phe	Cys	Leu	Glu	Ala	Leu	Lys	Leu	Thr	Thr	Lys	Leu	Gln	Ile	Pro
	1010					1015					1020				
Arg	Gln	Cys	Ala	Leu	Phe	Leu	Val	Leu	Lys	Gly	Glu	Leu	Glu	Leu	Ala
1025					1030					1035					1040
Arg	Asn	Asp	Ile	Asp	Leu	Cys	Gln	Ser	Asp	Leu	Gln	Gln	Val	Leu	Phe
			1045						1050					1055	
Leu	Leu	Glu	Ser	Cys	Thr	Glu	Phe	Gly	Gly	Val	Thr	Gln	His	Leu	Asp
		1060						1065					1070		
Ser	Val	Lys	Lys	Val	His	Leu	Gln	Lys	Gly	Lys	Gln	Gln	Ala	Gln	Val
	1075						1080					1085			
Pro	Cys	Pro	Pro	Gln	Leu	Pro	Glu	Glu	Glu	Leu	Phe	Leu	Arg	Gly	Pro
	1090					1095					1100				
Ala	Leu	Glu	Leu	Val	Ala	Thr	Val	Ala	Lys	Glu	Pro	Gly	Pro	Ile	Ala
1105					1110					1115					1120
Pro	Ser	Thr	Asn	Ser	Ser	Pro	Val	Leu	Lys	Thr	Lys	Pro	Gln	Pro	Ile
			1125						1130					1135	
Pro	Asn	Phe	Leu	Ser	His	Ser	Pro	Thr	Cys	Asp	Cys	Ser	Leu	Cys	Ala
			1140					1145					1150		
Ser	Pro	Val	Leu	Thr	Ala	Val	Cys	Leu	Arg	Trp	Val	Leu	Val	Thr	Ala
		1155					1160					1165			

Gly Val Arg Leu Ala Met Gly His Gln Ala Gln Gly Leu Asp Leu Leu
 1170 1175 1180
 Gln Val Val Leu Lys Gly Cys Pro Glu Ala Ala Glu Arg Leu Thr Gln
 1185 1190 1195 1200
 Ala Leu Gln Ala Ser Leu Asn His Lys Thr Pro Pro Ser Leu Val Pro
 1205 1210 1215
 Ser Leu Leu Asp Glu Ile Leu Ala Gln Ala Tyr Thr Leu Leu Ala Leu
 1220 1225 1230
 Glu Gly Leu Asn Gln Pro Ser Asn Glu Ser Leu Gln Lys Val Leu Gln
 1235 1240 1245
 Ser Gly Leu Lys Phe Val Ala Ala Arg Ile Pro His Leu Glu Pro Trp
 1250 1255 1260
 Arg Ala Ser Leu Leu Leu Ile Trp Ala Leu Thr Lys Leu Gly Gly Leu
 1265 1270 1275 1280
 Ser Cys Cys Thr Thr Gln Leu Phe Ala Ser Ser Trp Gly Trp Gln Pro
 1285 1290 1295
 Pro Leu Ile Lys Ser Val Pro Gly Ser Glu Pro Ser Lys Thr Gln Gly
 1300 1305 1310
 Gln Lys Arg Ser Gly Arg Gly Arg Gln Lys Leu Ala Ser Ala Pro Leu
 1315 1320 1325
 Ser Leu Asn Asn Thr Ser Gln Lys Gly Leu Glu Gly Arg Gly Leu Pro
 1330 1335 1340
 Cys Thr Pro Lys Pro Pro Asp Arg Ile Arg Gln Ala Gly Pro His Val
 1345 1350 1355 1360
 Pro Phe Thr Val Phe Glu Glu Val Cys Pro Thr Glu Ser Lys Pro Glu
 1365 1370 1375
 Val Pro Gln Ala Pro Arg Val Gln Gln Arg Val Gln Thr Arg Leu Lys
 1380 1385 1390
 Val Asn Phe Ser Asp Asp Ser Asp Leu Glu Asp Pro Val Ser Ala Glu
 1395 1400 1405
 Ala Trp Leu Ala Glu Glu Pro Lys Arg Arg Gly Thr Ala Ser Arg Gly
 1410 1415 1420
 Arg Gly Arg Ala Arg Lys Gly Leu Ser Leu Lys Thr Asp Ala Val Val
 1425 1430 1435 1440
 Ala Pro Gly Ser Ala Pro Gly Asn Pro Gly Leu Asn Gly Arg Ser Arg
 1445 1450 1455
 Arg Ala Lys Lys Val Ala Ser Arg His Cys Glu Glu Arg Arg Pro Gln
 1460 1465 1470
 Arg Ala Ser Asp Gln Ala Arg Pro Gly Pro Glu Ile Met Arg Thr Ile
 1475 1480 1485
 Pro Glu Glu Glu Leu Thr Asp Asn Trp Arg Lys Met Ser Phe Glu Ile
 1490 1495 1500

Leu Arg Gly Ser Asp Gly Glu Asp Ser Ala Ser Gly Gly Lys Thr Pro
 1505 1510 1515 1520
 Ala Pro Gly Pro Glu Ala Ala Ser Gly Glu Trp Glu Leu Leu Arg Leu
 1525 1530 1535
 Asp Ser Ser Lys Lys Lys Leu Pro Ser Pro Cys Pro Asp Lys Glu Ser
 1540 1545 1550
 Asp Lys Asp Leu Gly Pro Arg Leu Gln Leu Pro Ser Ala Pro Val Ala
 1555 1560 1565
 Thr Gly Leu Ser Thr Leu Asp Ser Ile Cys Asp Ser Leu Ser Val Ala
 1570 1575 1580
 Phe Arg Gly Ile Ser His Cys Pro Pro Ser Gly Leu Tyr Ala His Leu
 1585 1590 1595 1600
 Cys Arg Phe Leu Ala Leu Cys Leu Gly His Arg Asp Pro Tyr Ala Thr
 1605 1610 1615
 Ala Phe Leu Val Thr Glu Ser Val Ser Ile Thr Cys Arg His Gln Leu
 1620 1625 1630
 Leu Thr His Leu His Arg Gln Leu Ser Lys Ala Gln Lys His Arg Gly
 1635 1640 1645
 Ser Leu Glu Ile Ala Asp Gln Leu Gln Gly Leu Ser Leu Gln Glu Met
 1650 1655 1660
 Pro Gly Asp Val Pro Leu Ala Arg Ile Gln Arg Leu Phe Ser Phe Arg
 1665 1670 1675 1680
 Ala Leu Glu Ser Gly His Phe Pro Gln Pro Glu Lys Glu Ser Phe Gln
 1685 1690 1695
 Glu Arg Leu Ala Leu Ile Pro Ser Gly Val Thr Val Cys Val Leu Ala
 1700 1705 1710
 Leu Ala Thr Leu Gln Pro Gly Thr Val Gly Asn Thr Leu Leu Leu Thr
 1715 1720 1725
 Arg Leu Glu Lys Asp Ser Pro Pro Val Ser Val Gln Ile Pro Thr Gly
 1730 1735 1740
 Gln Asn Lys Leu His Leu Arg Ser Val Leu Asn Glu Phe Asp Ala Ile
 1745 1750 1755 1760
 Gln Lys Ala Gln Lys Glu Asn Ser Ser Cys Thr Asp Lys Arg Glu Trp
 1765 1770 1775
 Trp Thr Gly Arg Leu Ala Leu Asp His Arg Met Glu Val Leu Ile Ala
 1780 1785 1790
 Ser Leu Glu Lys Ser Val Leu Gly Cys Trp Lys Gly Leu Leu Leu Pro
 1795 1800 1805
 Ser Ser Glu Glu Pro Gly Pro Ala Gln Glu Ala Ser Arg Leu Gln Glu
 1810 1815 1820
 Leu Leu Gln Asp Cys Gly Trp Lys Tyr Pro Asp Arg Thr Leu Leu Lys
 1825 1830 1835 1840

Ile Met Leu Ser Gly Ala Gly Ala Leu Thr Pro Gln Asp Ile Gln Ala
 1845 1850 1855
 Leu Ala Tyr Gly Leu Cys Pro Thr Gln Pro Glu Arg Ala Gln Glu Leu
 1860 1865 1870
 Leu Asn Glu Ala Val Gly Arg Leu Gln Gly Leu Thr Val Pro Ser Asn
 1875 1880 1885
 Ser His Leu Val Leu Val Leu Asp Lys Asp Leu Gln Lys Leu Pro Trp
 1890 1895 1900
 Glu Ser Met Pro Ser Leu Gln Ala Leu Pro Val Thr Arg Leu Pro Ser
 1905 1910 1915 1920
 Phe Arg Phe Leu Leu Ser Tyr Ser Ile Ile Lys Glu Tyr Gly Ala Ser
 1925 1930 1935
 Pro Val Leu Ser Gln Gly Val Asp Pro Arg Ser Thr Phe Tyr Val Leu
 1940 1945 1950
 Asn Pro His Asn Asn Leu Ser Ser Thr Glu Glu Gln Phe Arg Ala Asn
 1955 1960 1965
 Phe Ser Ser Glu Ala Gly Trp Arg Gly Val Val Gly Glu Val Pro Arg
 1970 1975 1980
 Pro Glu Gln Val Gln Glu Ala Leu Thr Lys His Asp Leu Tyr Ile Tyr
 1985 1990 1995 2000
 Ala Gly His Gly Ala Gly Ala Arg Phe Leu Asp Gly Gln Ala Val Leu
 2005 2010 2015
 Arg Leu Ser Cys Arg Ala Val Ala Leu Leu Phe Gly Cys Ser Ser Ala
 2020 2025 2030
 Ala Leu Ala Val His Gly Asn Leu Glu Gly Ala Gly Ile Val Leu Lys
 2035 2040 2045
 Tyr Ile Met Ala Gly Cys Pro Leu Phe Leu Gly Asn Leu Trp Asp Val
 2050 2055 2060
 Thr Asp Arg Asp Ile Asp Arg Tyr Thr Glu Ala Leu Leu Gln Gly Trp
 2065 2070 2075 2080
 Leu Gly Ala Gly Pro Gly Ala Pro Leu Leu Tyr Tyr Val Asn Gln Ala
 2085 2090 2095

Arg Gln Ala Pro Arg Leu Lys Tyr Leu Ile Gly Ala Ala Pro Ile Ala
 2100 2105 2110

Tyr Gly Leu Pro Val Ser Leu Arg
 2115 2120

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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33

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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24

<210> 5

<211> 54

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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54

<210> 6

<211> 55

<212> DNA

<213> Artificial Sequence

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55

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<211> 56

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

<400> 7

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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[illegible]